

SEQUENCE LISTING

<110> Jomaa, Hassan

<120> Process for identifying chemical active ingredients and active ingredients for inhibiting the 1-deoxy-D-xylulose-5-phosphate biosynthesis pathway

<130> 15514

<140> PCT/EP99/02463

<141> 1999-04-13

<150> DE19843279.8

<151> 1998-09-22

<150> DE19816196.4

<151> 1998-04-14

<150> DE19828097.1

<151> 1998-06-24

<150> DE19825585.3

<151> 1998-06-09

<150> DE19831637.2

<151> 1998-07-15

<150> DE19831639.9

<151> 1998-07-15

<150> DE19831638.0

<151> 1998-07-15

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 1467

<212> DNA

<213> Plasmodium falciparum

<220>

<221> mRNA

<222> (1)..(1467)

<220>

<221> gene

<222> (1)..(1467)

<220>

<221> CDS

<222> (1)..(1467)

<400> 1

atg aag aaa tat att tat ata tat ttt ttc ttc atc aca ata act att 48  
Met Lys Lys Tyr Ile Tyr Ile Tyr Phe Phe Phe Ile Thr Ile Thr Ile  
1 5 10 15

aat gat tta gta ata aat aat aca tca aaa tgt gtt tcc att gaa aga 96  
Asn Asp Leu Val Ile Asn Asn Thr Ser Lys Cys Val Ser Ile Glu Arg  
20 25 30

aga aaa aat aac gca tat ata aat tat ggt ata gga tat aat gga cca 144  
Arg Lys Asn Asn Ala Tyr Ile Asn Tyr Gly Ile Gly Tyr Asn Gly Pro  
35 40 45

gat aat aaa ata aca aag agt aga aga tgt aaa aga ata aag tta tgc 192  
Asp Asn Lys Ile Thr Lys Ser Arg Arg Cys Lys Arg Ile Lys Leu Cys  
50 55 60

aaa aag gat tta ata gat att ggt gca ata aag aaa cca att aat gta 240  
Lys Lys Asp Leu Ile Asp Ile Gly Ala Ile Lys Lys Pro Ile Asn Val  
65 70 75 80

gca att ttt gga agt act ggt agt ata ggt acg aat gct tta aat ata 288  
Ala Ile Phe Gly Ser Thr Gly Ser Ile Gly Thr Asn Ala Leu Asn Ile  
85 90 95

ata agg gag tgt aat aaa att gaa aat gtt ttt aat gtt aaa gca ttg 336  
Ile Arg Glu Cys Asn Lys Ile Glu Asn Val Phe Asn Val Lys Ala Leu  
100 105 110

tat gtg aat aag agt gtg aat gaa tta tat gaa caa gct aga gaa ttt 384  
Tyr Val Asn Lys Ser Val Asn Glu Leu Tyr Glu Gln Ala Arg Glu Phe  
115 120 125

tta cca gaa tat ttg tgt ata cat gat aaa agt gta tat gaa gaa tta 432  
Leu Pro Glu Tyr Leu Cys Ile His Asp Lys Ser Val Tyr Glu Glu Leu  
130 135 140

aaa gaa ctg gta aaa aat ata aaa gat tat aaa cct ata ata ttg tgt 480  
Lys Glu Leu Val Lys Asn Ile Lys Asp Tyr Lys Pro Ile Ile Leu Cys  
145 150 155 160

ggt gat gaa ggg atg aaa gaa ata tgt agt aat agt ata gat aaa			528
Gly Asp Glu Gly Met Lys Glu Ile Cys Ser Ser Asn Ser Ile Asp Lys			
165	170	175	
ata gtt att ggt att gat tct ttt caa gga tta tat tct act atg tat			576
Ile Val Ile Gly Ile Asp Ser Phe Gln Gly Leu Tyr Ser Thr Met Tyr			
180	185	190	
gca att atg aat aat aaa ata gtt gcg tta gct aat aaa gaa tcc att			624
Ala Ile Met Asn Asn Lys Ile Val Ala Leu Ala Asn Lys Glu Ser Ile			
195	200	205	
gtc tct gct ggt ttc ttt tta aag aaa tta tta aat att cat aaa aat			672
Val Ser Ala Gly Phe Phe Leu Lys Lys Leu Leu Asn Ile His Lys Asn			
210	215	220	
gca aag ata ata cct gtt gat tca gaa cat agt gct ata ttt caa tgt			720
Ala Lys Ile Ile Pro Val Asp Ser Glu His Ser Ala Ile Phe Gln Cys			
225	230	235	240
tta gat aat aat aag gta tta aaa aca aaa tgt tta caa gac aat ttt			768
Leu Asp Asn Asn Lys Val Leu Lys Thr Lys Cys Leu Gln Asp Asn Phe			
245	250	255	
tct aaa att aac aat ata aat aaa ata ttt tta tgt tca tct gga ggt			816
Ser Lys Ile Asn Asn Ile Asn Lys Ile Phe Leu Cys Ser Ser Gly Gly			
260	265	270	
cca ttt caa aat tta act atg gac gaa tta aaa aat gta aca tca gaa			864
Pro Phe Gln Asn Leu Thr Met Asp Glu Leu Lys Asn Val Thr Ser Glu			
275	280	285	
aat gct tta aag cat cct aaa tgg aaa atg ggt aag aaa ata act ata			912
Asn Ala Leu Lys His Pro Lys Trp Lys Met Gly Lys Lys Ile Thr Ile			
290	295	300	
gat tct gca act atg atg aat aaa ggt tta gag gtt ata gaa acc cat			960
Asp Ser Ala Thr Met Met Asn Lys Gly Leu Glu Val Ile Glu Thr His			
305	310	315	320
ttt tta ttt gat gta gat tat aat gat ata gaa gtt ata gta cat aaa			1008
Phe Leu Phe Asp Val Asp Tyr Asn Asp Ile Glu Val Ile Val His Lys			
325	330	335	
gaa tgc att ata cat tct tgt gtt gaa ttt ata gac aaa tca gta ata			1056
Glu Cys Ile Ile His Ser Cys Val Glu Phe Ile Asp Lys Ser Val Ile			
340	345	350	

agt caa atg tat tat cca gat atg caa ata ccc ata tta tat tct tta	1104		
Ser Gln Met Tyr Tyr Pro Asp Met Gln Ile Pro Ile Leu Tyr Ser Leu	-		
355	360	365	
aca tgg cct gat aga ata aaa aca aat tta aaa cct tta gat ttg gct	1152		
Thr Trp Pro Asp Arg Ile Lys Thr Asn Leu Lys Pro Leu Asp Leu Ala			
370	375	380	
cag gtt tca act ctt aca ttt cat aaa cct tct tta gaa cat ttc ccg	1200		
Gln Val Ser Thr Leu Thr Phe His Lys Pro Ser Leu Glu His Phe Pro			
385	390	395	400
tgt att aaa tta gct tat caa gca ggt ata aaa gga aac ttt tat cca	1248		
Cys Ile Lys Leu Ala Tyr Gln Ala Gly Ile Lys Gly Asn Phe Tyr Pro			
405	410	415	
act gta cta aat gcg tca aat gaa ata gct aac aac tta ttt ttg aat	1296		
Thr Val Leu Asn Ala Ser Asn Glu Ile Ala Asn Asn Leu Phe Leu Asn			
420	425	430	
aat aaa att aaa tat ttt gat att tcc tct ata ata tcg caa gtt ctt	1344		
Asn Lys Ile Lys Tyr Phe Asp Ile Ser Ser Ile Ile Ser Gln Val Leu			
435	440	445	
gaa tct ttc aat tct caa aag gtt tcg gaa aat agt gaa gat tta atg	1392		
Glu Ser Phe Asn Ser Gln Lys Val Ser Glu Asn Ser Glu Asp Leu Met			
450	455	460	
aag caa att cta caa ata cat tct tgg gcc aaa gat aaa gct acc gat	1440		
Lys Gln Ile Leu Gln Ile His Ser Trp Ala Lys Asp Lys Ala Thr Asp			
465	470	475	480
ata tac aac aaa cat aat tct tca tag	1467		
Ile Tyr Asn Lys His Asn Ser Ser			
485			

<210> 2  
 <211> 488  
 <212> PRT  
 <213> Plasmodium falciparum

<400> 2  
 Met Lys Lys Tyr Ile Tyr Ile Tyr Phe Phe Phe Ile Thr Ile Thr Ile  
 1 5 10 15  
 Asn Asp Leu Val Ile Asn Asn Thr Ser Lys Cys Val Ser Ile Glu Arg  
 20 25 30

Arg Lys Asn Asn Ala Tyr Ile Asn Tyr Gly Ile Gly Tyr Asn Gly Pro  
35 40 45

Asp Asn Lys Ile Thr Lys Ser Arg Arg Cys Lys Arg Ile Lys Leu Cys  
50 55 60

Lys Lys Asp Leu Ile Asp Ile Gly Ala Ile Lys Lys Pro Ile Asn Val  
65 70 75 80

Ala Ile Phe Gly Ser Thr Gly Ser Ile Gly Thr Asn Ala Leu Asn Ile  
85 90 95

Ile Arg Glu Cys Asn Lys Ile Glu Asn Val Phe Asn Val Lys Ala Leu  
100 105 110

Tyr Val Asn Lys Ser Val Asn Glu Leu Tyr Glu Gln Ala Arg Glu Phe  
115 120 125

Leu Pro Glu Tyr Leu Cys Ile His Asp Lys Ser Val Tyr Glu Glu Leu  
130 135 140

Lys Glu Leu Val Lys Asn Ile Lys Asp Tyr Lys Pro Ile Ile Leu Cys  
145 150 155 160

Gly Asp Glu Gly Met Lys Glu Ile Cys Ser Ser Asn Ser Ile Asp Lys  
165 170 175

Ile Val Ile Gly Ile Asp Ser Phe Gln Gly Leu Tyr Ser Thr Met Tyr  
180 185 190

Ala Ile Met Asn Asn Lys Ile Val Ala Leu Ala Asn Lys Glu Ser Ile  
195 200 205

Val Ser Ala Gly Phe Phe Leu Lys Lys Leu Leu Asn Ile His Lys Asn  
210 215 220

Ala Lys Ile Ile Pro Val Asp Ser Glu His Ser Ala Ile Phe Gln Cys  
225 230 235 240

Leu Asp Asn Asn Lys Val Leu Lys Thr Lys Cys Leu Gln Asp Asn Phe  
245 250 255

Ser Lys Ile Asn Asn Ile Asn Lys Ile Phe Leu Cys Ser Ser Gly Gly  
. 260 265 270

Pro Phe Gln Asn Leu Thr Met Asp Glu Leu Lys Asn Val Thr Ser Glu  
275 280 285

Asn Ala Leu Lys His Pro Lys Trp Lys Met Gly Lys Lys Ile Thr Ile  
290 295 300

Asp Ser Ala Thr Met Met Asn Lys Gly Leu Glu Val Ile Glu Thr His  
305 310 315 320

Phe Leu Phe Asp Val Asp Tyr Asn Asp Ile Glu Val Ile Val His Lys  
325 330 335

Glu Cys Ile Ile His Ser Cys Val Glu Phe Ile Asp Lys Ser Val Ile  
340 345 350

Ser Gln Met Tyr Tyr Pro Asp Met Gln Ile Pro Ile Leu Tyr Ser Leu  
355 360 365

Thr Trp Pro Asp Arg Ile Lys Thr Asn Leu Lys Pro Leu Asp Leu Ala  
370 375 380

Gln Val Ser Thr Leu Thr Phe His Lys Pro Ser Leu Glu His Phe Pro  
385 390 395 400

Cys Ile Lys Leu Ala Tyr Gln Ala Gly Ile Lys Gly Asn Phe Tyr Pro  
405 410 415

Thr Val Leu Asn Ala Ser Asn Glu Ile Ala Asn Asn Leu Phe Leu Asn  
420 425 430

Asn Lys Ile Lys Tyr Phe Asp Ile Ser Ser Ile Ile Ser Gln Val Leu  
435 440 445

Glu Ser Phe Asn Ser Gln Lys Val Ser Glu Asn Ser Glu Asp Leu Met  
450 455 460

Lys Gln Ile Leu Gln Ile His Ser Trp Ala Lys Asp Lys Ala Thr Asp  
465 470 475 480

Ile Tyr Asn Lys His Asn Ser Ser  
485

<210> 3  
<211> 3872  
<212> DNA  
<213> Plasmodium falciparum

<220>

<221> CDS

<222> (126)..(3740)

<220>

<221> gene

<222> (1)..(3872)

<220>

<221> mRNA

<222> (1)..(3872)

<400> 3

ggtaatatac gtataatata tatataatat attcttacgt atgtatcatt tatgaatcat 60

aataatattc taaatttacc ttccgtttt gctcgatctt ctcatttcg tttcagctt 120

tatca atg att ttt aat tat gtg ttt ttt aag aac ttt gta cca gtt gtt 170

Met Ile Phe Asn Tyr Val Phe Phe Lys Asn Phe Val Pro Val Val

1

5

10

15

ctat tac att ctc ctt ata ata tat att aac tta aat ggc atg aat aat 218

Leu Tyr Ile Leu Leu Ile Ile Tyr Ile Asn Leu Asn Gly Met Asn Asn

20

25

30

aaa aat caa ata aaa aca gaa aaa att tat ata aag aaa ttg aat agg 266

Lys Asn Gln Ile Lys Thr Glu Lys Ile Tyr Ile Lys Lys Leu Asn Arg

35

40

45

ttg tca agg aaa aat tcg tta tgt agt tct aaa aat aaa ata gca tgc 314

Leu Ser Arg Lys Asn Ser Leu Cys Ser Ser Lys Asn Lys Ile Ala Cys

50

55

60

ttg ttc gat ata gga aat gat gat aat aga aat acg aca tat ggc tat 362

Leu Phe Asp Ile Gly Asn Asp Asp Asn Arg Asn Thr Thr Tyr Gly Tyr

65

70

75

aat gtg aat gtt aaa aat gat gat att aat tcc tta cta aaa aat aat 410

Asn Val Asn Val Lys Asn Asp Asp Ile Asn Ser Leu Leu Lys Asn Asn

80

85

90

95

tat agt aat aaa ttg tac atg gat aag agg aaa aat att aat aat gta 458

Tyr Ser Asn Lys Leu Tyr Met Asp Lys Arg Lys Asn Ile Asn Asn Val

100

105

110

att agt act aat aaa ata tct ggg tcc att tca aat att tgt agt aga 506

Ile Ser Thr Asn Lys Ile Ser Gly Ser Ile Ser Asn Ile Cys Ser Arg

115

120

125

aat caa aaa gaa aat gaa caa aaa aga aat aaa caa aga tgt tta act	554
Asn Gln Lys Glu Asn Glu Gln Lys Arg Asn Lys Gln Arg Cys Leu Thr	
130 135 140	
caa tgt cac act tat aat atg tca cat gaa cag gac aaa cta gct aat	602
Gln Cys His Thr Tyr Asn Met Ser His Glu Gln Asp Lys Leu Ala Asn	
145 150 155	
gat aat aat agg aat aat aaa aag aat ttt aat tta tta ttt ata aat	650
Asp Asn Asn Arg Asn Asn Lys Lys Asn Phe Asn Leu Leu Phe Ile Asn	
160 165 170 175	
tat ttt aat ttg aaa cga atg aaa aat tct ctt cta aat aaa gac aat	698
Tyr Phe Asn Leu Lys Arg Met Lys Asn Ser Leu Leu Asn Lys Asp Asn	
180 185 190	
ttc ttt tac tgt aaa gaa aaa aaa ttg tca ttt ctg cat aag gcc tat	746
Phe Phe Tyr Cys Lys Glu Lys Leu Ser Phe Leu His Lys Ala Tyr	
195 200 205	
aaa aaa aaa aat tgc act ttt caa aat tat agt tta aaa aga aaa tct	794
Lys Lys Asn Cys Thr Phe Gln Asn Tyr Ser Leu Lys Arg Lys Ser	
210 215 220	
aat cgt gat tca cat aaa ttg ttt tct gga gaa ttt gac gat tat aca	842
Asn Arg Asp Ser His Lys Leu Phe Ser Gly Glu Phe Asp Asp Tyr Thr	
225 230 235	
aat aat aat gct tta tat gaa tcc gaa aaa aaa gaa tac att aca cta	890
Asn Asn Asn Ala Leu Tyr Glu Ser Glu Lys Lys Glu Tyr Ile Thr Leu	
240 245 250 255	
aat aat aat aat aaa aat aat aat aat aat aat gat aat aat aaa aat	938
Asn Asn Asn Asn Lys Asn Asn Asn Lys Asn Asn Asp Asn Lys Asn	
260 265 270	
aat gat aat aat gat tat aat aat aat aat agt tgt aat aat tta gga	986
Asn Asp Asn Asn Asp Tyr Asn Asn Asn Ser Cys Asn Asn Leu Gly	
275 280 285	
gag aga tcc aat cat tat gat aat tat ggt gga gat aat aat aat cca	1034
Glu Arg Ser Asn His Tyr Asp Asn Tyr Gly Gly Asp Asn Asn Asn Pro	
290 295 300	
tgt aat aat aat aat gac aaa tat gat ata gga aaa tat ttc aaa cag	1082
Cys Asn Asn Asn Asp Lys Tyr Asp Ile Gly Lys Tyr Phe Lys Gln	
305 310 315	

att aat acc ttt att aat att gat gaa tat aaa act ata tat ggt gat Ile Asn Thr Phe Ile Asn Ile Asp Glu Tyr Lys Thr Ile Tyr Gly Asp	320	325	330	335	1130
gaa ata tat aaa gaa ata tat gaa cta tat gta gaa aga aat att cct Glu Ile Tyr Lys Glu Ile Tyr Glu Leu Tyr Val Glu Arg Asn Ile Pro	340	345	350		1178
gaa tat tat gaa cga aaa tat ttt tca gaa gat att aaa aag agt gtc Glu Tyr Tyr Glu Arg Lys Tyr Phe Ser Glu Asp Ile Lys Lys Ser Val	355	360	365		1226
cta ttt gat ata gat aaa tat aat gat gtc gaa ttt gaa aaa gct ata Leu Phe Asp Ile Asp Lys Tyr Asn Asp Val Glu Phe Glu Lys Ala Ile	370	375	380		1274
aaa gaa gaa ttt ata aat aat gga gtt tat att aat aat ata gat aat Lys Glu Glu Phe Ile Asn Asn Gly Val Tyr Ile Asn Asn Ile Asp Asn	385	390	395		1322
aca tat tat aaa aaa gaa aat att tta ata atg aaa aag ata tta cat Thr Tyr Tyr Lys Lys Glu Asn Ile Leu Ile Met Lys Lys Ile Leu His	400	405	410	415	1370
tat ttc cca tta tta aaa tta att aat aat cca tca gat tta aaa aag Tyr Phe Pro Leu Leu Lys Leu Ile Asn Asn Pro Ser Asp Leu Lys Lys	420	425	430		1418
tta aaa aaa caa tat tta cct tta tta gca cat gaa tta aaa ata ttt Leu Lys Lys Gln Tyr Leu Pro Leu Leu Ala His Glu Leu Lys Ile Phe	435	440	445		1466
tta ttt ttt att gta aat ata aca gga ggt cat ttt tcc tct gtt tta Leu Phe Phe Ile Val Asn Ile Thr Gly Gly His Phe Ser Ser Val Leu	450	455	460		1514
agc tct tta gaa att caa tta tta ttg tat att ttt aat caa cca Ser Ser Leu Glu Ile Gln Leu Leu Leu Tyr Ile Phe Asn Gln Pro	465	470	475		1562
tat gat aat gtt ata tat gat ata gga cat caa gca tat gta cat aag Tyr Asp Asn Val Ile Tyr Asp Ile Gly His Gln Ala Tyr Val His Lys	480	485	490	495	1610
ata ttg acc gga aga aaa cta tta ttt cta tca tta aga aat aaa aaa Ile Leu Thr Gly Arg Lys Leu Leu Phe Leu Ser Leu Arg Asn Lys Lys	500	505	510		1658

ggt att agt gga ttc cta aat att ttt gaa agt att tat gat aaa ttt			1706
Gly Ile Ser Gly Phe Leu Asn Ile Phe Glu Ser Ile Tyr Asp Lys Phe			
515	520	525	
ggg gct ggt cac agt tcc act tca tta agt gct ata caa gga tat tat			1754
Gly Ala Gly His Ser Ser Thr Ser Leu Ser Ala Ile Gln Gly Tyr Tyr			
530	535	540	
gaa gcc gag tgg caa gtg aag aat aaa gaa aaa tat gga aat gga gat			1802
Glu Ala Glu Trp Gln Val Lys Asn Lys Glu Lys Tyr Gly Asn Gly Asp			
545	550	555	
ata gaa ata agt gat aac gca aat gtc acg aat aat gaa agg ata ttt			1850
Ile Glu Ile Ser Asp Asn Ala Asn Val Thr Asn Asn Glu Arg Ile Phe			
560	565	570	575
caa aaa gga ata cac aat gat aat aat att aac aat aat att aat aat			1898
Gln Lys Gly Ile His Asn Asp Asn Asn Ile Asn Asn Asn Ile Asn Asn			
580	585	590	
aat aat tat atc aat cct tca gat gtg gta gga aga gaa aat acg aat			1946
Asn Asn Tyr Ile Asn Pro Ser Asp Val Val Gly Arg Glu Asn Thr Asn			
595	600	605	
gta cca aat gta cga aat gat aac cat aac gtg gat aaa gta cac att			1994
Val Pro Asn Val Arg Asn Asp Asn His Asn Val Asp Lys Val His Ile			
610	615	620	
gct att ata gga gat ggt ggt tta aca ggt gga atg gca tta gaa gcg			2042
Ala Ile Ile Gly Asp Gly Gly Leu Thr Gly Gly Met Ala Leu Glu Ala			
625	630	635	
tta aat tat att tca ttc ttg aat tct aaa att tta att att tat aat			2090
Leu Asn Tyr Ile Ser Phe Leu Asn Ser Lys Ile Leu Ile Ile Tyr Asn			
640	645	650	655
gat aac gga caa gtt tct tta cca aca aat gcc gta agt ata tca ggt			2138
Asp Asn Gly Gln Val Ser Leu Pro Thr Asn Ala Val Ser Ile Ser Gly			
660	665	670	
aat aga cct ata ggt tct ata tca gat cat tta cat tat ttt gtt tct			2186
Asn Arg Pro Ile Gly Ser Ile Ser Asp His Leu His Tyr Phe Val Ser			
675	680	685	
aat ata gaa gca aat gct ggt gat aat aaa tta tcg aaa aat gca aaa			2234
Asn Ile Glu Ala Asn Ala Gly Asp Asn Lys Leu Ser Lys Asn Ala Lys			
690	695	700	

gag aat aac att ttt gaa aat ttg aat tat gat tat att ggt gtt gtg			2282
Glu Asn Asn Ile Phe Glu Asn Leu Asn Tyr Asp Tyr Ile Gly Val Val			
705	710	715	
aat ggt aat aat aca gaa gag ctc ttt aaa gta tta aat aat ata aaa			2330
Asn Gly Asn Asn Thr Glu Glu Leu Phe Lys Val Leu Asn Asn Ile Lys			
720	725	730	735
gaa aat aaa tta aaa aga gct act gtt ctt cat gta cgt aca aaa aaa			2378
Glu Asn Lys Leu Lys Arg Ala Thr Val Leu His Val Arg Thr Lys Lys			
740	745	750	
tcg aat gat ttt ata aat tca aag agt cca ata agt ata ttg cac tct			2426
Ser Asn Asp Phe Ile Asn Ser Lys Ser Pro Ile Ser Ile Leu His Ser			
755	760	765	
ata aag aaa aat gag att ttc cct ttc gat acc act ata tta aat gga			2474
Ile Lys Asn Glu Ile Phe Pro Phe Asp Thr Thr Ile Leu Asn Gly			
770	775	780	
aat att cat aag gag aac aag ata gaa gaa gag aaa aat ggt tct tca			2522
Asn Ile His Lys Glu Asn Lys Ile Glu Glu Glu Lys Asn Val Ser Ser			
785	790	795	
tct aca aag tat gat gta aat aat aag aat aat aaa aat aat gat aat			2570
Ser Thr Lys Tyr Asp Val Asn Asn Lys Asn Asn Lys Asn Asp Asn			
800	805	810	815
agt gaa att ata aaa tat gaa gat atg ttt tca aaa gag acg ttc aca			2618
Ser Glu Ile Ile Lys Tyr Glu Asp Met Phe Ser Lys Glu Thr Phe Thr			
820	825	830	
gat ata tat aca aat gaa atg tta aaa tat tta aag aaa gat aga aat			2666
Asp Ile Tyr Thr Asn Glu Met Leu Lys Tyr Leu Lys Lys Asp Arg Asn			
835	840	845	
ata ata ttc cta tct ccc gct atg tta gga gga tca gga ttg gtt aaa			2714
Ile Ile Phe Leu Ser Pro Ala Met Leu Gly Gly Ser Gly Leu Val Lys			
850	855	860	
att agt gag cgt tat cca aat aat gta tat gat gta ggt ata gca gaa			2762
Ile Ser Glu Arg Tyr Pro Asn Asn Val Tyr Asp Val Gly Ile Ala Glu			
865	870	875	
caa cat tct gta act ttc gca gca gct atg gca atg aat aag aaa tta			2810
Gln His Ser Val Thr Phe Ala Ala Ala Met Ala Met Asn Lys Lys Leu			
880	885	890	895

aaa ata caa tta tgt ata tat tcg acc ttt tta caa aga gca tat gat Lys Ile Gln Leu Cys Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr Asp 900 905 910	2858
caa att ata cat gat ctt aat tta caa aat ata cct tta aag gtt ata Gln Ile Ile His Asp Leu Asn Leu Gln Asn Ile Pro Leu Lys Val Ile 915 920 925	2906
att gga aga agt gga tta gta gga gag gat ggg gca aca cat caa ggt Ile Gly Arg Ser Gly Leu Val Gly Glu Asp Gly Ala Thr His Gln Gly 930 935 940	2954
ata tat gat tta tct tat ctt ggg aca ctt aac aat gca tat ata ata Ile Tyr Asp Leu Ser Tyr Leu Gly Thr Leu Asn Asn Ala Tyr Ile Ile 945 950 955	3002
tct cca agt aat caa gtt gat ttg aaa aga gct ctt agg ttt gct tat Ser Pro Ser Asn Gln Val Asp Leu Lys Arg Ala Leu Arg Phe Ala Tyr 960 965 970 975	3050
tta gat aag gac cat tct gtg tat ata cgt ata ccc aga atg aac ata Leu Asp Lys Asp His Ser Val Tyr Ile Arg Ile Pro Arg Met Asn Ile 980 985 990	3098
tta agt gat aag tac atg aaa gga tat ttg aac att cat atg aaa aat Leu Ser Asp Lys Tyr Met Lys Gly Tyr Leu Asn Ile His Met Lys Asn 995 1000 1005	3146
gag agc aaa aat atc gat gta aac gtg gat ata aac gat gat gta gat Glu Ser Lys Asn Ile Asp Val Asn Val Asp Ile Asn Asp Asp Val Asp 1010 1015 1020	3194
aaa tat agt gaa gaa tat atg gac gat gat aat ttt ata aaa tcg ttt Lys Tyr Ser Glu Glu Tyr Met Asp Asp Asp Asn Phe Ile Lys Ser Phe 1025 1030 1035	3242
att gga aaa tct aga att att aaa atg gat aat gaa aat aat aca Ile Gly Lys Ser Arg Ile Ile Lys Met Asp Asn Glu Asn Asn Asn Thr 1040 1045 1050 1055	3290
aat gaa cat tat tca agc aga gga gat aca cag aca aaa aaa aaa aaa Asn Glu His Tyr Ser Ser Arg Gly Asp Thr Gln Thr Lys Lys Lys Lys 1060 1065 1070	3338
gtt tgt atc ttt aac atg ggt agt atg ctt ttt aat gta att aat gct Val Cys Ile Phe Asn Met Gly Ser Met Leu Phe Asn Val Ile Asn Ala 1075 1080 1085	3386

ata aaa gaa att gaa aaa gaa caa tat att tca cat aat tat tct ttt Ile Lys Glu Ile Glu Lys Glu Gln Tyr Ile Ser His Asn Tyr Ser Phe	1090	1095	1100	3434
tca att gtt gat atg ata ttt tta aat cct tta gat aaa aat atg ata Ser Ile Val Asp Met Ile Phe Leu Asn Pro Leu Asp Lys Asn Met Ile	1105	1110	1115	3482
gat cat gta ata aaa caa aat aaa cat caa tat tta att act tat gaa Asp His Val Ile Lys Gln Asn Lys His Gln Tyr Leu Ile Thr Tyr Glu	1120	1125	1130	1135
gat aat act ata ggt ggt ttt tct aca cat ttc aat aat tat tta ata Asp Asn Thr Ile Gly Gly Phe Ser Thr His Phe Asn Asn Tyr Leu Ile	1140	1145	1150	3578
gaa aat aat tat att aca aaa cat aac tta tat gtt cat aat att tat Glu Asn Asn Tyr Ile Thr Lys His Asn Leu Tyr Val His Asn Ile Tyr	1155	1160	1165	3626
tta tct aat gag cca att gaa cat gca tct ttt aag gat caa caa gaa Leu Ser Asn Glu Pro Ile Glu His Ala Ser Phe Lys Asp Gln Gln Glu	1170	1175	1180	3674
gtc gtc aaa atg gat aaa tgt agt ctt gtc aat aga att aaa aat tat Val Val Lys Met Asp Lys Cys Ser Leu Val Asn Arg Ile Lys Asn Tyr	1185	1190	1195	3722
ctt aaa aat aat cct aca tgatgttataaataataat tttctaaaat Leu Lys Asn Asn Pro Thr	1200	1205		3770
tatTTTTTT ttatacttta atgtgtacaa taaaatataat atctaaatataat tttttatTTG				3830
tacgcttttt tttttttttt tttaattgtt atttttgtat at				3872
<210> 4				
<211> 1205				
<212> PRT				
<213> Plasmodium falciparum				
<400> 4				
Met Ile Phe Asn Tyr Val Phe Phe Lys Asn Phe Val Pro Val Val Leu	1	5	10	15
Tyr Ile Leu Leu Ile Ile Tyr Ile Asn Leu Asn Gly Met Asn Asn Lys	20	25	30	

Asn Gln Ile Lys Thr Glu Lys Ile Tyr Ile Lys Lys Leu Asn Arg Leu  
35 40 45

Ser Arg Lys Asn Ser Leu Cys Ser Ser Lys Asn Lys Ile Ala Cys Leu  
50 55 60

Phe Asp Ile Gly Asn Asp Asp Asn Arg Asn Thr Thr Tyr Gly Tyr Asn  
65 70 75 80

Val Asn Val Lys Asn Asp Asp Ile Asn Ser Leu Leu Lys Asn Asn Tyr  
85 90 95

Ser Asn Lys Leu Tyr Met Asp Lys Arg Lys Asn Ile Asn Asn Val Ile  
100 105 110

Ser Thr Asn Lys Ile Ser Gly Ser Ile Ser Asn Ile Cys Ser Arg Asn  
115 120 125

Gln Lys Glu Asn Glu Gln Lys Arg Asn Lys Gln Arg Cys Leu Thr Gln  
130 135 140

Cys His Thr Tyr Asn Met Ser His Glu Gln Asp Lys Leu Ala Asn Asp  
145 150 155 160

Asn Asn Arg Asn Asn Lys Lys Asn Phe Asn Leu Leu Phe Ile Asn Tyr  
165 170 175

Phe Asn Leu Lys Arg Met Lys Asn Ser Leu Leu Asn Lys Asp Asn Phe  
180 185 190

Phe Tyr Cys Lys Glu Lys Lys Leu Ser Phe Leu His Lys Ala Tyr Lys  
195 200 205

Lys Lys Asn Cys Thr Phe Gln Asn Tyr Ser Leu Lys Arg Lys Ser Asn  
210 215 220

Arg Asp Ser His Lys Leu Phe Ser Gly Glu Phe Asp Asp Tyr Thr Asn  
225 230 235 240

Asn Asn Ala Leu Tyr Glu Ser Glu Lys Lys Glu Tyr Ile Thr Leu Asn  
245 250 255

Asn Asn Asn Lys Asn Asn Asn Lys Asn Asn Asp Asn Lys Asn Asn  
260 265 270

Asp Asn Asn Asp Tyr Asn Asn Asn Ser Cys Asn Asn Leu Gly Glu  
275 280 285

Arg Ser Asn His Tyr Asp Asn Tyr Gly Gly Asp Asn Asn Asn Pro Cys  
290 295 300

Asn Asn Asn Asn Asp Lys Tyr Asp Ile Gly Lys Tyr Phe Lys Gln Ile  
305 310 315 320

Asn Thr Phe Ile Asn Ile Asp Glu Tyr Lys Thr Ile Tyr Gly Asp Glu  
325 330 335

Ile Tyr Lys Glu Ile Tyr Glu Leu Tyr Val Glu Arg Asn Ile Pro Glu  
340 345 350

Tyr Tyr Glu Arg Lys Tyr Phe Ser Glu Asp Ile Lys Lys Ser Val Leu  
355 360 365

Phe Asp Ile Asp Lys Tyr Asn Asp Val Glu Phe Glu Lys Ala Ile Lys  
370 375 380

Glu Glu Phe Ile Asn Asn Gly Val Tyr Ile Asn Asn Ile Asp Asn Thr  
385 390 395 400

Tyr Tyr Lys Lys Glu Asn Ile Leu Ile Met Lys Lys Ile Leu His Tyr  
405 410 415

Phe Pro Leu Leu Lys Leu Ile Asn Asn Pro Ser Asp Leu Lys Lys Leu  
420 425 430

Lys Lys Gln Tyr Leu Pro Leu Leu Ala His Glu Leu Lys Ile Phe Leu  
435 440 445

Phe Phe Ile Val Asn Ile Thr Gly Gly His Phe Ser Ser Val Leu Ser  
450 455 460

Ser Leu Glu Ile Gln Leu Leu Leu Tyr Ile Phe Asn Gln Pro Tyr  
465 470 475 480

Asp Asn Val Ile Tyr Asp Ile Gly His Gln Ala Tyr Val His Lys Ile  
485 490 495

Leu Thr Gly Arg Lys Leu Leu Phe Leu Ser Leu Arg Asn Lys Lys Gly  
500 505 510

Ile Ser Gly Phe Leu Asn Ile Phe Glu Ser Ile Tyr Asp Lys Phe Gly  
515 520 525

Ala Gly His Ser Ser Thr Ser Leu Ser Ala Ile Gln Gly Tyr Tyr Glu  
530 535 540

Ala Glu Trp Gln Val Lys Asn Lys Glu Lys Tyr Gly Asn Gly Asp Ile  
545 550 555 560

Glu Ile Ser Asp Asn Ala Asn Val Thr Asn Asn Glu Arg Ile Phe Gln  
565 570 575

Lys Gly Ile His Asn Asp Asn Asn Ile Asn Asn Asn Ile Asn Asn Asn  
580 585 590

Asn Tyr Ile Asn Pro Ser Asp Val Val Gly Arg Glu Asn Thr Asn Val  
595 600 605

Pro Asn Val Arg Asn Asp Asn His Asn Val Asp Lys Val His Ile Ala  
610 615 620

Ile Ile Gly Asp Gly Gly Leu Thr Gly Gly Met Ala Leu Glu Ala Leu  
625 630 635 640

Asn Tyr Ile Ser Phe Leu Asn Ser Lys Ile Leu Ile Ile Tyr Asn Asp  
645 650 655

Asn Gly Gln Val Ser Leu Pro Thr Asn Ala Val Ser Ile Ser Gly Asn  
660 665 670

Arg Pro Ile Gly Ser Ile Ser Asp His Leu His Tyr Phe Val Ser Asn  
675 680 685

Ile Glu Ala Asn Ala Gly Asp Asn Lys Leu Ser Lys Asn Ala Lys Glu  
690 695 700

Asn Asn Ile Phe Glu Asn Leu Asn Tyr Asp Tyr Ile Gly Val Val Asn  
705 710 715 720

Gly Asn Asn Thr Glu Glu Leu Phe Lys Val Leu Asn Asn Ile Lys Glu  
725 730 735

Asn Lys Leu Lys Arg Ala Thr Val Leu His Val Arg Thr Lys Lys Ser  
740 745 750

Asn Asp Phe Ile Asn Ser Lys Ser Pro Ile Ser Ile Leu His Ser Ile  
755 760 765

Lys Lys Asn Glu Ile Phe Pro Phe Asp Thr Thr Ile Leu Asn Gly Asn  
770 775 780

Ile His Lys Glu Asn Lys Ile Glu Glu Glu Lys Asn Val Ser Ser Ser  
785 790 795 800

Thr Lys Tyr Asp Val Asn Asn Lys Asn Asn Lys Asn Asn Asp Asn Ser  
805 810 815

Glu Ile Ile Lys Tyr Glu Asp Met Phe Ser Lys Glu Thr Phe Thr Asp  
820 825 830

Ile Tyr Thr Asn Glu Met Leu Lys Tyr Leu Lys Lys Asp Arg Asn Ile  
835 840 845

Ile Phe Leu Ser Pro Ala Met Leu Gly Gly Ser Gly Leu Val Lys Ile  
850 855 860

Ser Glu Arg Tyr Pro Asn Asn Val Tyr Asp Val Gly Ile Ala Glu Gln  
865 870 875 880

His Ser Val Thr Phe Ala Ala Ala Met Ala Met Asn Lys Lys Leu Lys  
885 890 895

Ile Gln Leu Cys Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr Asp Gln  
900 905 910

Ile Ile His Asp Leu Asn Leu Gln Asn Ile Pro Leu Lys Val Ile Ile  
915 920 925

Gly Arg Ser Gly Leu Val Gly Glu Asp Gly Ala Thr His Gln Gly Ile  
930 935 940

Tyr Asp Leu Ser Tyr Leu Gly Thr Leu Asn Asn Ala Tyr Ile Ile Ser  
945 950 955 960

Pro Ser Asn Gln Val Asp Leu Lys Arg Ala Leu Arg Phe Ala Tyr Leu  
965 970 975

Asp Lys Asp His Ser Val Tyr Ile Arg Ile Pro Arg Met Asn Ile Leu  
980 985 990

Ser Asp Lys Tyr Met Lys Gly Tyr Leu Asn Ile His Met Lys Asn Glu  
995 1000 1005

Ser Lys Asn Ile Asp Val Asn Val Asp Ile Asn Asp Asp Val Asp Lys  
1010 1015 1020

Tyr Ser Glu Glu Tyr Met Asp Asp Asp Asn Phe Ile Lys Ser Phe Ile  
1025 1030 1035 1040

Gly Lys Ser Arg Ile Ile Lys Met Asp Asn Glu Asn Asn Asn Thr Asn  
1045 1050 1055

Glu His Tyr Ser Ser Arg Gly Asp Thr Gln Thr Lys Lys Lys Lys Val  
1060 1065 1070

Cys Ile Phe Asn Met Gly Ser Met Leu Phe Asn Val Ile Asn Ala Ile  
1075 1080 1085

Lys Glu Ile Glu Lys Glu Gln Tyr Ile Ser His Asn Tyr Ser Phe Ser  
1090 1095 1100

Ile Val Asp Met Ile Phe Leu Asn Pro Leu Asp Lys Asn Met Ile Asp  
105 1110 1115 1120

His Val Ile Lys Gln Asn Lys His Gln Tyr Leu Ile Thr Tyr Glu Asp  
1125 1130 1135

Asn Thr Ile Gly Gly Phe Ser Thr His Phe Asn Asn Tyr Leu Ile Glu  
1140 1145 1150

Asn Asn Tyr Ile Thr Lys His Asn Leu Tyr Val His Asn Ile Tyr Leu  
1155 1160 1165

Ser Asn Glu Pro Ile Glu His Ala Ser Phe Lys Asp Gln Gln Glu Val  
1170 1175 1180

Val Lys Met Asp Lys Cys Ser Leu Val Asn Arg Ile Lys Asn Tyr Leu  
1185 1190 1195 1200

Lys Asn Asn Pro Thr  
1205